SEQUENCE LISTING

<110> Zhang, Lian-Hui
      Dong, Yihu
      Xu, Jinling

<120> Global Regulators of Bacterial Pathogenic Genes as Targets for
      Engineering Disease Resistance

<130> 2977-127

<140> US 10/019,661
<141> 2002-04-29

<150> PCT/SG99/00128
<151> 1999-11-17

<150> SG 9903146-0
<151> 1999-07-02

<160> 4

<170> PatentIn version 3.2

<210> 1
<211> 1222
<212> DNA
<213> Bacillus sp.

<400> 1
ctttactgta ttgttttatt caaaactaaa tgtaaaggtg gatacataat gacagtaaag   60

aagctttatt tcgtcccagc aggtcgttgt atgttggatc attcgtctgt taatagtaca   120

ttaacaccag gagaattatt agacttaccg gtttggtgtt atcttttgga gactgaagaa   180

ggacctattt tagtagatac aggtatgcca gaaagtgcag ttaataatga aggtcttttt   240

aacggtacat ttgtcgaagg gcaggtttta ccgaaaatga ctgaagaaga tagaatcgtg   300

aatattttaa aacgggttgg ttatgagccg gaagaccttc tttatattat tagttctcac   360

ttgcattttg atcatgcagg aggaaatggc gcttttataa atacaccaat cattgtacag   420

cgtgctgaat atgaggcggc gcagcatagc gaagaatatt tgaaagaatg tatattgccg   480

aatttaaact acaaaatcat tgaaggtgat tatgaagtcg taccaggagt tcaattattg   540

catacaccag gccatactcc agggcatcaa tcgctattaa ttgagacaga aaaatccggt   600

cctgtattat taacgattga tgcatcgtat acgaaagaga attttgaaaa tgaagtgcca   660

```
tttgcgggat ttgattcaga attagcttta tcttcaatta aacgtttaaa agaagtggtg      720

atgaaagaga agccgattgt tttctttgga catgatatag agcaggaaag gggatgtaaa      780

gtgttccctg aatatatata gtacaaaaag tcatgagctt attcgctcat gactttttcg      840

tttaaatgat tttttttaaat aagttataaa cttttttaga actatcttca tttaattgat      900

agtacgtaag gtttacatca ttaggagtat cttgttgagc aatcatcact tcgttactgt      960

gatggtcaac tacccatatg aaatattttt tataagtccc atcctcgaaa gtaatccaca     1020

tatcacagtc tattaaatct gatccttctt catctaatgt taattttcct tttttggcgg     1080

tatccatact gttaatgaat gttttttaatt catctgtttt tgtgagaaag atatcctttt     1140

ttgtttttaat tgactcgaca tgtatatctt ttatttcttg ttttcctaaa aagacagggg     1200

gctcatttgg gtctctttga gt                                              1222
```

```
<210>   2
<211>   250
<212>   PRT
<213>   Bacillus sp.

<400>   2

Met Thr Val Lys Lys Leu Tyr Phe Val Pro Ala Gly Arg Cys Met Leu
1               5                   10                  15


Asp His Ser Ser Val Asn Ser Thr Leu Thr Pro Gly Glu Leu Leu Asp
            20                  25                  30


Leu Pro Val Trp Cys Tyr Leu Leu Glu Thr Glu Glu Gly Pro Ile Leu
        35                  40                  45


Val Asp Thr Gly Met Pro Glu Ser Ala Val Asn Asn Glu Gly Leu Phe
    50                  55                  60


Asn Gly Thr Phe Val Glu Gly Gln Val Leu Pro Lys Met Thr Glu Glu
65                  70                  75                  80


Asp Arg Ile Val Asn Ile Leu Lys Arg Val Gly Tyr Glu Pro Glu Asp
                85                  90                  95
```

Leu Leu Tyr Ile Ile Ser Ser His Leu His Phe Asp His Ala Gly Gly
            100   105   110

Asn Gly Ala Phe Ile Asn Thr Pro Ile Ile Val Gln Arg Ala Glu Tyr
            115   120   125

Glu Ala Ala Gln His Ser Glu Glu Tyr Leu Lys Glu Cys Ile Leu Pro
        130   135   140

Asn Leu Asn Tyr Lys Ile Ile Glu Gly Asp Tyr Glu Val Val Pro Gly
145   150   155   160

Val Gln Leu Leu His Thr Pro Gly His Thr Pro Gly His Gln Ser Leu
                165   170   175

Leu Ile Glu Thr Glu Lys Ser Gly Pro Val Leu Leu Thr Ile Asp Ala
            180   185   190

Ser Tyr Thr Lys Glu Asn Phe Glu Asn Glu Val Pro Phe Ala Gly Phe
            195   200   205

Asp Ser Glu Leu Ala Leu Ser Ser Ile Lys Arg Leu Lys Glu Val Val
        210   215   220

Met Lys Glu Lys Pro Ile Val Phe Phe Gly His Asp Ile Glu Gln Glu
225   230   235   240

Arg Gly Cys Lys Val Phe Pro Glu Tyr Ile
                245   250

<210>   3
<211>   12
<212>   PRT
<213>   Bacillus sp.

<400>   3

Ile Leu Val Asp Thr Gly Met Pro Glu Ser Ala Val
1   5   10

<210>   4

```
<211>  12
<212>  PRT
<213>  artificial

<220>
<223>  consensus aspartyl proteases active site motif


<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  X= LIVMFGA or C

<220>
<221>  MISC_FEATURE
<222>  (2)..(2)
<223>  X= LIVMTAD or N

<220>
<221>  MISC_FEATURE
<222>  (3)..(3)
<223>  X= LIVFS or A

<220>
<221>  MISC_FEATURE
<222>  (5)..(5)
<223>  X= S or T

<220>
<221>  MISC_FEATURE
<222>  (7)..(7)
<223>  X= STA or V

<220>
<221>  MISC_FEATURE
<222>  (8)..(8)
<223>  X= STAPDEN or Q

<220>
<221>  MISC_FEATURE
<222>  (9)..(9)
<223>  X= any amino acid

<220>
<221>  MISC_FEATURE
<222>  (10)..(10)
<223>  X= LIVMFSTN or C

<220>
<221>  MISC_FEATURE
<222>  (11)..(11)
<223>  X= any amino acid
```

```
<220>
<221>  MISC_FEATURE
<222>  (12)..(12)
<223>  X= LIVMFGT or A

<400>  4

Xaa Xaa Xaa Asp Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10
```